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—
Fig.

1101	CCCTTGACTC	CTGGGAGCC	CTCATGAGGA	AGTTGGCCT	CATGCCAAT	GAGATAAGC	TGGCTAAAGC	TGAGGAGCG	GGCCACAGGG	ACACCTTGTA
1102	GAAACTGAG	GACCCTGGC	GACTACTCT	TCACCCGGG	GTACTGTAA	CTCTATTTC	ACCGATTTC	ACTCCGTCG	CCGGTGTCCC	TGTGGAAACAT
322	Phe	Asp	Pro	Leu	Met	Arg	Leu	Leu	Leu	Leu
1201	CACCGATGCTG	ATAAAGTGGG	TCAACAAAC	CGGGCGAGAT	GCCTCTGTCC	ACACCCCTGCT	GGATGCCCTTG	GAGACGCTGG	GAGAGAGACT	TGCCAAGCGAG
355	GTGCTAGAC	TATTTCACCC	AGTTGTTTG	GGCCGCTCTA	CGGAGACAGG	TGTGGGACGAA	CCTACGGAAAC	CTCTGGGACC	CTCTCTCTGA	ACGGTGTGTC
	Thr	Met	Leu	Ile	Lys	Leu	Ala	Ala	Ala	Ala
1301	AAGATTGAGG	ACCACTGTT	GAGCTCTGGA	AAGTTCATGT	ATCTAGAAGG	TAATGCCAGAC	TCTGCCWTGT	CCTAAGGTGTG	ATTCTCTTCA	GGAAGTGTGAGA
388	TCTTAACTCC	TGGTGAAACAA	CTCGAGACCT	TTCAACTACA	TAGATCTTCC	ATTACGTCTG	AGACGGAAACA	GGATTACAC	TAAGAGAAGT	CCTTCACTCT
	Lys	Ile	Leu	Lys	Leu	Ala	Leu	Leu	Leu	Leu
1401	CCTTCCCTGG	TTTACCTTT	TTCTGGAAAA	AGCCCAACTG	GAECTCCAGTC	AGTAGGAAAG	TGCCACAAATT	GTCACTGAC	CGGTACTGGG	AGAAAPCTCTC
	GGAAAGGGACC	AAATGGAAA	AAGACCTTT	TCGGGTTGAC	CTGAGGTCA	TCATCCCTTC	ACGGTGTAA	CAGTGTACTG	GCATGACCT	TCTTTGAGAG
1501	CCATCCAACA	TCACCCAGTG	GATGGAACAT	CCCTGTAACCT	TTCACTGCA	TTGGCATATT	TTTATAAGC	TGAATGTGAT	AATAAGGACA	CTATGGAAT
	GGTAGGTGT	AGTGGGTCA	CTACCTGTA	GGACATTGAA	AAGTGACGT	AACCGTAATA	AAAATATTG	ACTTACACTA	TTATTCCCTGT	GATACTTTA
1601	GTCTGGATCA	TTGGGATCA	GGGTACTTTG	AGATTGGTT	TGGGATGTCA	TTGGTTTCAC	AGCACTTTT	TATCCTTAATG	TAATGCTT	ATTATTTAT
	CAGACCTGT	AAGGCAAAAC	TCTAAACCA	ACCCCTACGT	AACAAAGTG	TGGTGA	AAAAAA	ATAGGATTAC	ATTACGAAA	AAATAAATAA
1701	TTGGGCTACA	TTGTAAGATC	CATCTACAA	AAAAAAAGAA	GGGGGGGGG	ACTCTAGAGT	CGACCTGGCAG	AACTCTGGCC	GGCATGGCC	CGGTACCGG
	AACCCGATGT	AACTTCTAG	GTAGATGTTT	TTTTTTTTTT	TTTTTTTTTC	CCGGCGGGC	TGAGATCTCA	GCTGGACGTC	TTCGAACCCGG	CGGTACCGG

Fig. 1 (cont.)

Fig. 2 A

1 MEORGONAPAASGARKRHPGPREARGARGPLRVPKTLVLLVVAVLLVSAESALITQD
 61 LAPQQRAAPQQKRSSPSEGLCPPGHEHISEDGRDCISCKYQDYSTHWNDLILFCRLRCTRD
 121 SGEVELSPCTTRNTVCOCEEGTFREEDSPMEMCRKCRTGCPGMVKVGDCTPWSDIEQVH
 181 KESGIIIGVTVAAVLLIVAVFVCKSSLWKKVLPYLGICSGGGGDPERVDRSSQRPGAEQD
 241 NVLNEIVSILQOPTQVPEQEMEVQEPAEPTGVNMLSPGESEHLEPAEAERSQRRLVPA
 301 NEGDPTETLRQCFFDFADLVPFDSWEPILMRKLGLMDNEIKVAKAAAGHRDTLYTMLIKW
 361 VNKTGRDASVHTLDALETLGERLAKOKEIQLLSSGKFMYLEGNADSALS

Fig. 2 B

APO2	DR4	APO3/DR3	TNFR1	Fas/Apo1
YTHWVNKITGRD - ASVHTULDALETLGEFLAKQKIED	YAMMVKYQKGRN - ASIHDIDDALEMEERHAKERKIQD	YEMIKRVRQOQ - - AGT GAVYAALELERNQEDGCVEDLRS	YSMLATNRRRTPRERATEELIGRVIRRDMDILGCLEDIEE	YOLLNWYQLLHGGKKEAY - DDIKDEKKANECTLAEEKQT

Fig. 3

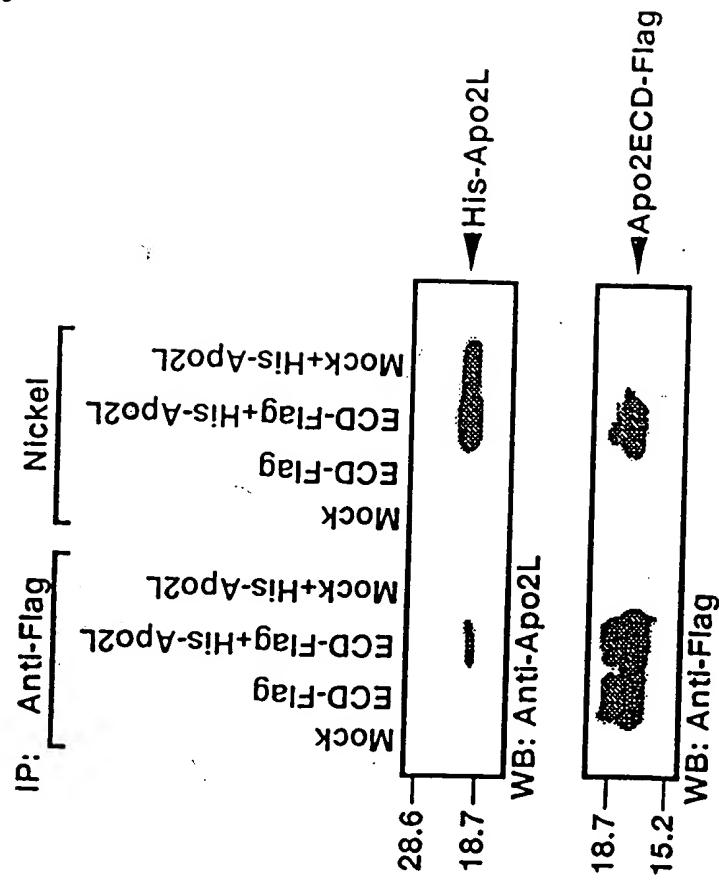
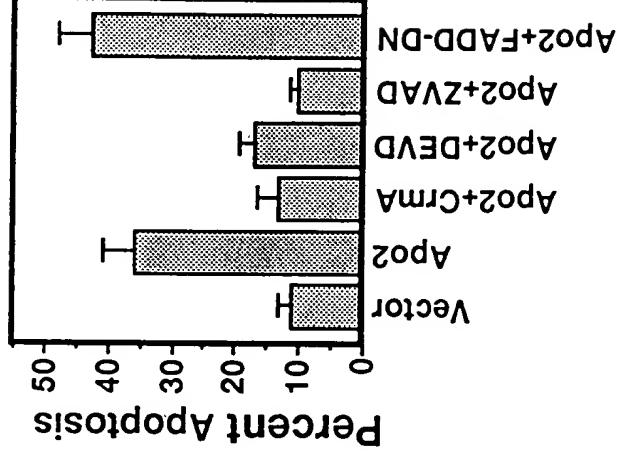
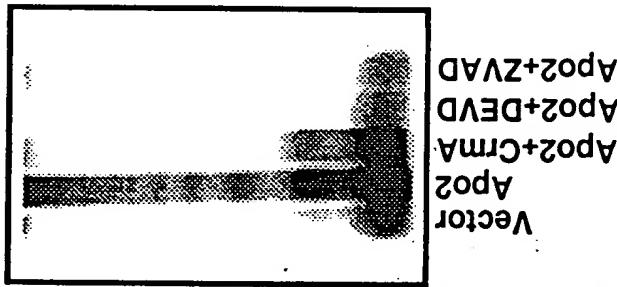


Fig. 4

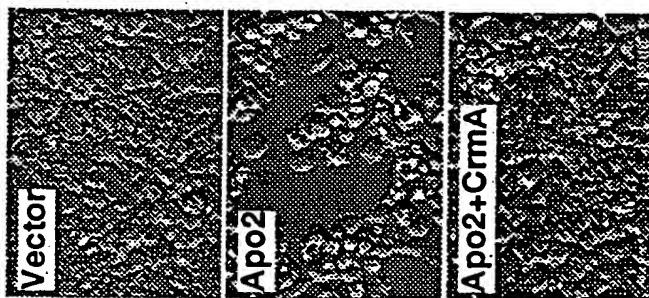
4C



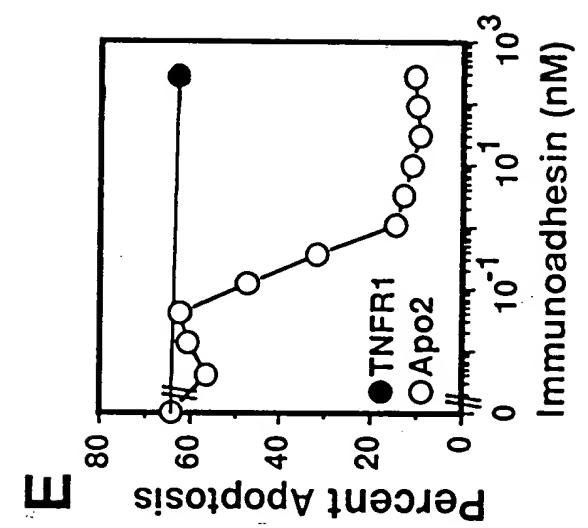
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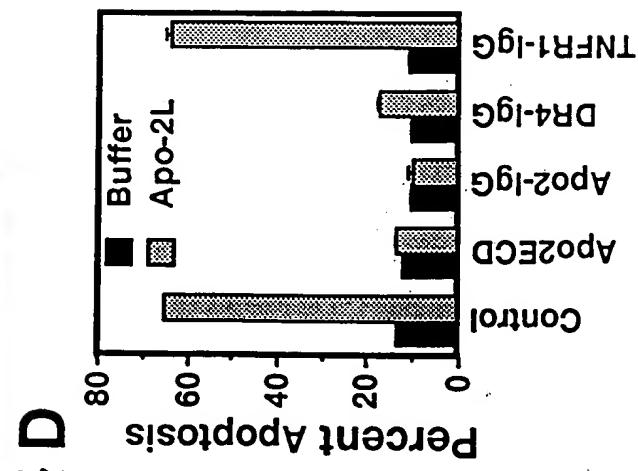
4A

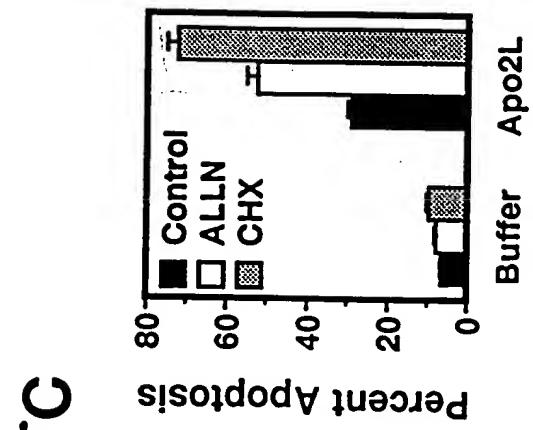


4E



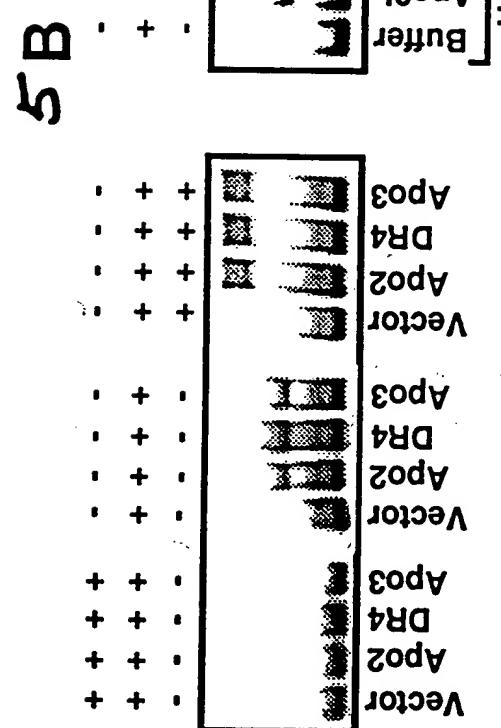
4D





Percent Apoptosis

5C

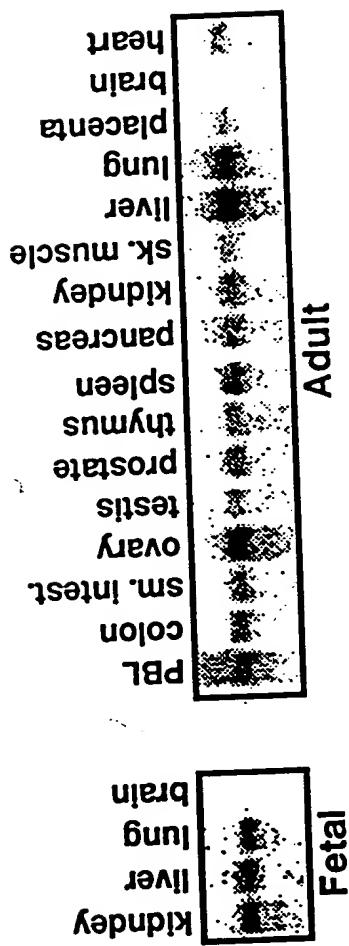


5A

Anti-p65	Unlabelled probe	Labelled probe
-	-	-
+	+	+
+	+	+
+	+	+
+	+	+
+	+	+
-	-	-
+	+	+
+	+	+
+	+	+
+	+	+
+	+	+
-	-	-
+	+	+
+	+	+
+	+	+
+	+	+
+	+	+
-	-	-

Fig. 5

FIG. 6



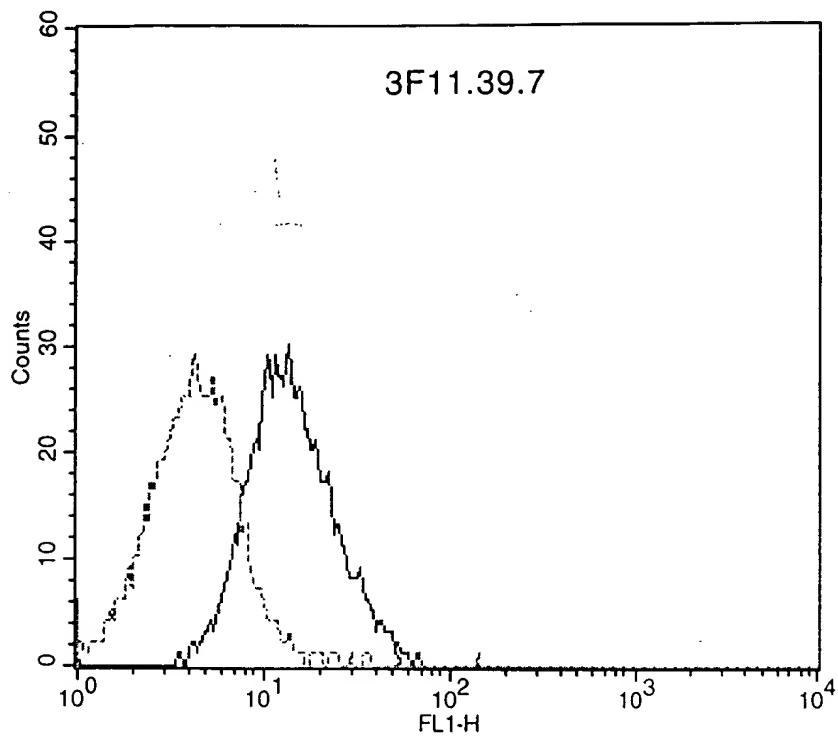


Fig. 7

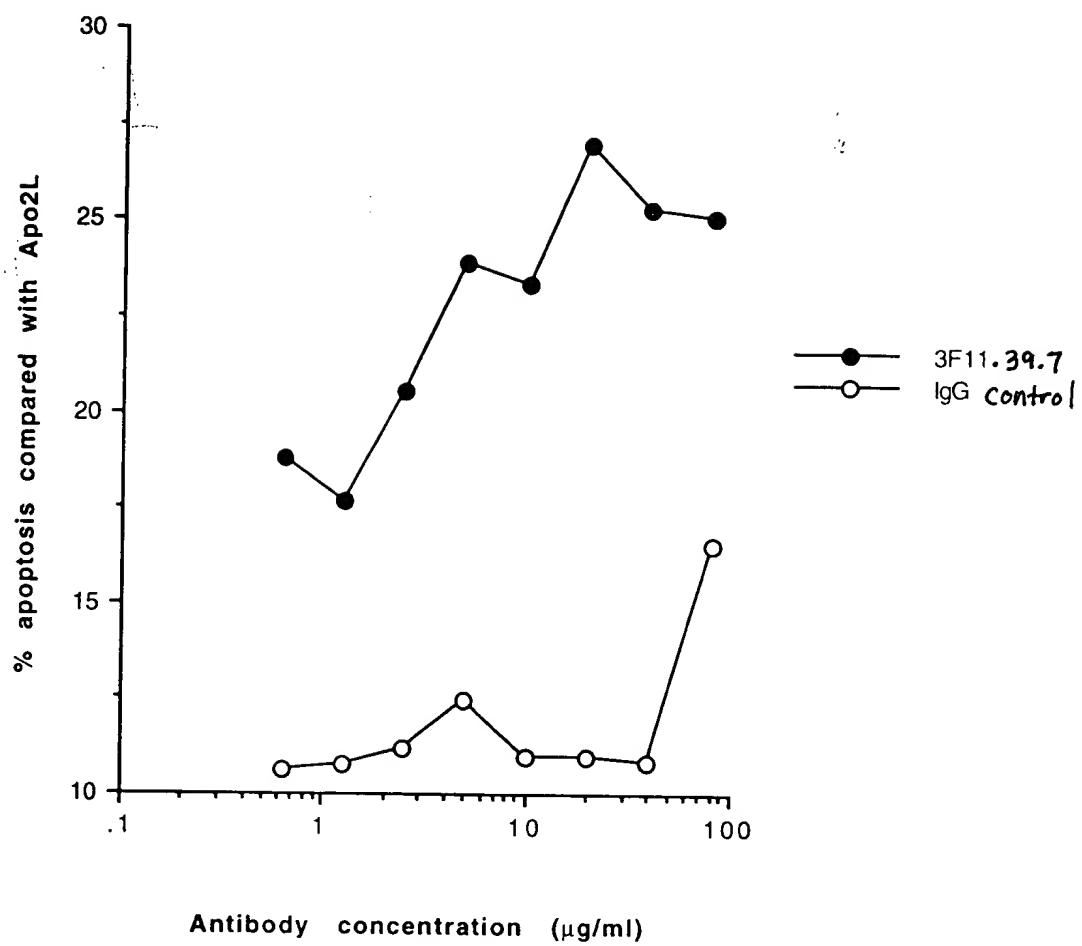


Fig. 8

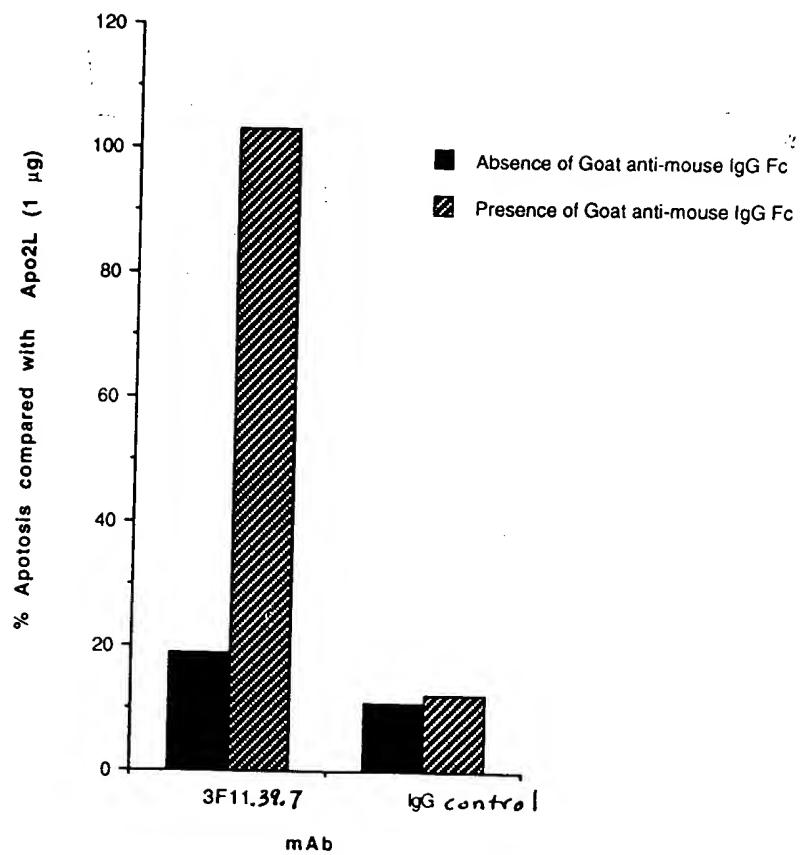


Fig. 9

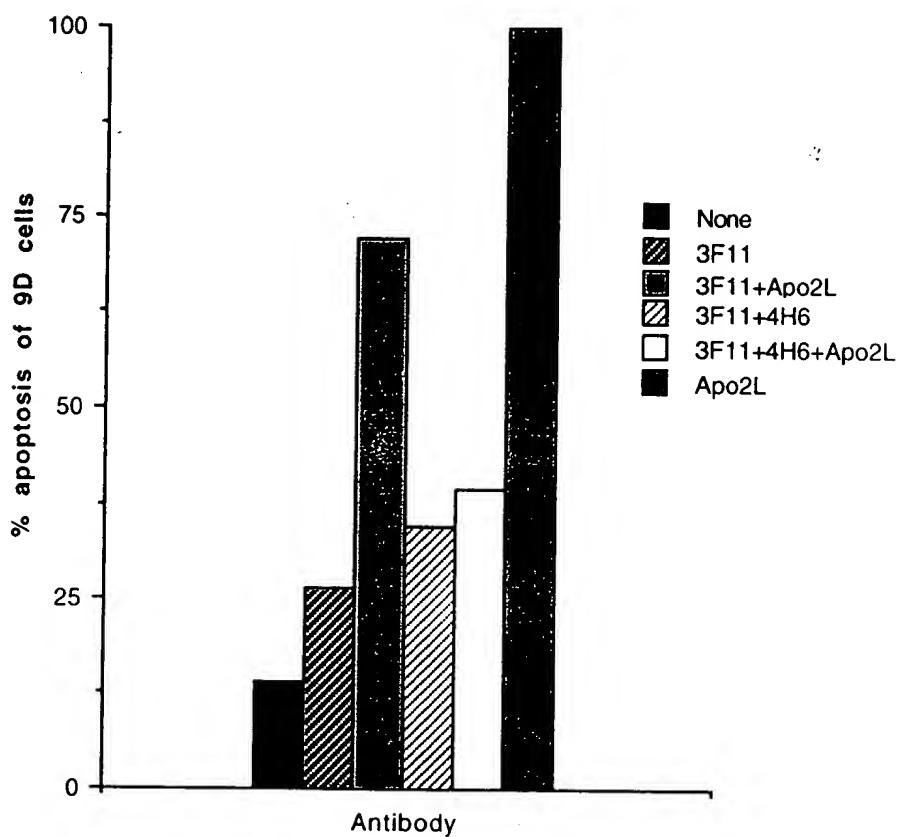


Fig. 10

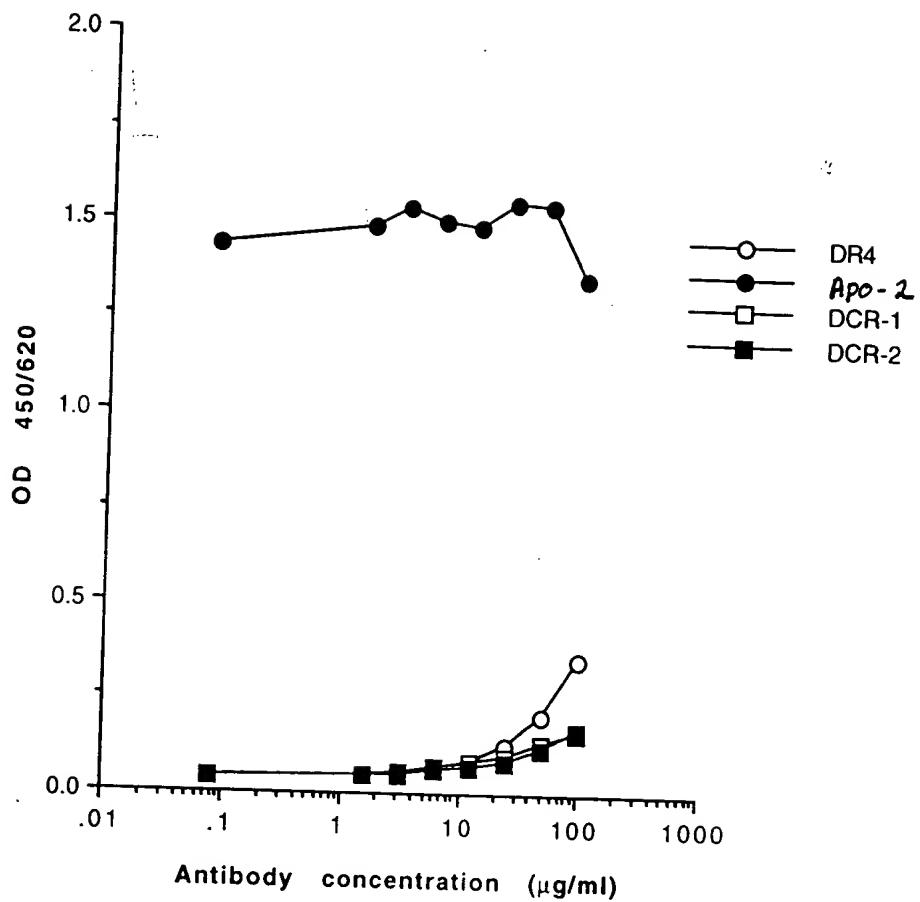


Fig. 11